



Initial assembled sequence  
[Strand]

1 AGAAAATACC CACTTTCTCA GGATGATATC AATGGAATCC AGTCCATCTA TGGAGGTCTG  
61 CCTAAGGAAC CTGCTAAGCC AAAGGAACCC ACTATACCCC ATGCCTGTGA CCCTGACTTG  
121 ACTTTTGACG CTATCACAAC TTTCCGCAGA GAAGTAATGT TCTTTAAAGG CAGGCACCTA  
181 TGGAGGATCT ATTATGATAT CACGGATGTT GAGTTTGAAT TAATTGCTTC ATTCTGGCCA  
241 TCTCTGCCAG CTGATCTGCA AGCTGCATAC GAGAACCCCA GAGATAAGAT TCTGGTTTTT  
301 AAAGATGAAA ACTTCTGGAT GATCAGAGGA TATGCTGTCT TGCCAGATTA TCCCAAATCC  
361 ATCCATACAT TAGGTTTTCC AGGACGTGTG AAGAAAATAG ATGCAGCCGT CTGTGATAAG  
421 ACCACAAGAA AAACCTACTT CTTTGTGGGC ATTTGGTGCT GGAGGTTTGA TGAAATGACC  
481 CAAACCATGG ACAAAGGGTT CCCGCAGAGA GTGGTAAAC ACTTTCCTGG AATCAGTATC  
541 CGTGTTGATG CTGCTTTCCA GTACAAAGGA TTCTTCTTTT TCAGCCGTGG ATCAACGCAA  
601 TTTGAATACG ACATTAAGAC AAAGAATATT ACCCGAATCA TGAGAACTAA TACTTGGTTT  
661 CAATGCAAAG AACCAAAGAA CTCCTCATTT GGTTTTGATA TCAACAAGGA AAAAGCACAT  
721 TCAGGAGGCA TAAAGATATT GTATCATAAG AGTTTAAGCT TGTTTATTTT TGGTATTGTT  
781 CATTTGCTGA AAAACACTTC TATTTATCAA TAAATTCATA GACCTAAAAT AAA

*Fig. 1*

gaaagagagg a atg aag cgc ctt ctg ctt ctg ttt ttg ttc ttt ata aca 50  
Met Lys Arg Leu Leu Leu Leu Phe Leu Phe Phe Ile Thr  
 1 5 10

ttt tct tct gca ttt ccc tta gtc cgg atg atg gaa aat gaa gaa aat 98  
Phe Ser Ser Ala Phe Pro Leu Val Arg Met Met Glu Asn Glu Glu Asn  
 15 20 25

gtg caa ctg gct cag gca tat ctc aac cag ttc tac tct ctt gaa ata 146  
 Val Gln Leu Ala Gln Ala Tyr Leu Asn Gln Phe Tyr Ser Leu Glu Ile  
 30 35 40 45

gaa ggg aat cat ctt gtt caa agc aag aat agg agt ctc ata gat gac 194  
 Glu Gly Asn His Leu Val Gln Ser Lys Asn Arg Ser Leu Ile Asp Asp  
 50 55 60

aaa att cgg gaa atg caa gca ttt ttt gga ttg aca gtg act gga aga 242  
 Lys Ile Arg Glu Met Gln Ala Phe Phe Gly Leu Thr Val Thr Gly Arg  
 65 70 75

ctg gac tca aac acc ctt gag atc atg aag aca ccc agg tgt ggg gtg 290  
 Leu Asp Ser Asn Thr Leu Glu Ile Met Lys Thr Pro Arg Cys Gly Val  
 80 85 90

cct gat gtg ggc cag tat ggc tac acc ctc cct ggg tgg aga aaa tac 338  
Pro Asp Val Gly Gln Tyr Gly Tyr Thr Leu Pro Gly Trp Arg Lys Tyr  
 95 100 105

aac ctc acc tac aga ata ata aac tat act ccg gat atg gca cga gct 386  
 Asn Leu Thr Tyr Arg Ile Ile Asn Tyr Thr Pro Asp Met Ala Arg Ala  
 110 115 120 125

gct gtg gat gag gct atc caa gaa ggt tta gaa gtg tgg agc aaa gtc 434  
 Ala Val Asp Glu Ala Ile Gln Glu Gly Leu Glu Val Trp Ser Lys Val  
 130 135 140

act cca cta aaa ttc acc aag att tca aag ggg att gca gac atc atg 482  
 Thr Pro Leu Lys Phe Thr Lys Ile Ser Lys Gly Ile Ala Asp Ile Met  
 145 150 155

*Fig. 2A*

att gcc ttt agg act cga gtc cat ggt cgg tgt cct cgc tat ttt gat	530
Ile Ala Phe Arg Thr Arg Val His Gly Arg Cys Pro Arg Tyr Phe Asp	
160 165 170	
ggt ccc ttg gga gtt ctt ggc cat gcc ttt cct cct ggt ccg ggt ctg	578
Gly Pro Leu Gly Val Leu Gly His Ala Phe Pro Pro Gly Pro Gly Leu	
175 180 185	
ggt ggt gac act cat ttt gat gag gat gaa aac tgg acc aag gat gga	626
Gly Gly Asp Thr His Phe Asp Glu Asp Glu Asn Trp Thr Lys Asp Gly	
190 195 200 205	
gca gga ttc aac ttg ttt ctt gtg gct gct cat gaa ttt ggt cat gca	674
Ala Gly Phe Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ala	
210 215 220	
ctg ggg ctc tct cac tcc aat gat caa aca gcc ttg atg ttc cca aat	722
Leu Gly Leu Ser His Ser Asn Asp Gln Thr Ala Leu Met Phe Pro Asn	
225 230 235	
tat gtc tcc ctg gat ccc aga aaa tac cca ctt tct cag gat gat atc	770
Tyr Val Ser Leu Asp Pro Arg Lys Tyr Pro Leu Ser Gln Asp Asp Ile	
240 245 250	
aat gga atc cag tcc atc tat gga ggt ctg cct aag gaa cct gct aag	818
Asn Gly Ile Gln Ser Ile Tyr Gly Gly Leu Pro Lys Glu Pro Ala Lys	
255 260 265	
cca aag gaa ccc act ata ccc cat gcc tgt gac cct gac ttg act ttt	866
Pro Lys Glu Pro Thr Ile Pro His Ala Cys Asp Pro Asp Leu Thr Phe	
270 275 280 285	
gac gct atc aca act ttc cgc aga gaa gta atg ttc ttt aaa ggc agg	914
Asp Ala Ile Thr Thr Phe Arg Arg Glu Val Met Phe Phe Lys Gly Arg	
290 295 300	
cac cta tgg agg atc tat tat gat atc acg gat gtt gag ttt gaa tta	962
His Leu Trp Arg Ile Tyr Tyr Asp Ile Thr Asp Val Glu Phe Glu Leu	
305 310 315	

*Fig. 2B*

att gct tca ttc tgg cca tct ctg cca gct gat ctg caa gct gca tac 1010  
 Ile Ala Ser Phe Trp Pro Ser Leu Pro Ala Asp Leu Gln Ala Ala Tyr  
 320 325 330

gag aac ccc aga gat aag att ctg gtt ttt aaa gat gaa aac ttc tgg 1058  
 Glu Asn Pro Arg Asp Lys Ile Leu Val Phe Lys Asp Glu Asn Phe Trp  
 335 340 345

atg atc aga gga tat gct gtc ttg cca gat tat ccc aaa tcc atc cat 1106  
 Met Ile Arg Gly Tyr Ala Val Leu Pro Asp Tyr Pro Lys Ser Ile His  
 350 355 360 365

aca tta ggt ttt cca gga cgt gtg aag aaa ata gat gca gcc gtc tgt 1154  
 Thr Leu Gly Phe Pro Gly Arg Val Lys Lys Ile Asp Ala Ala Val Cys  
 370 375 380

gat aag acc aca aga aaa acc tac ttc ttt gtg ggc att tgg tgc tgg 1202  
 Asp Lys Thr Thr Arg Lys Thr Tyr Phe Phe Val Gly Ile Trp Cys Trp  
 385 390 395

agg ttt gat gaa atg acc caa acc atg gac aaa ggg ttc ccg cag aga 1250  
 Arg Phe Asp Glu Met Thr Gln Thr Met Asp Lys Gly Phe Pro Gln Arg  
 400 405 410

gtg gta aaa cac ttt cct gga atc agt atc cgt gtt gat gct gct ttc 1298  
 Val Val Lys His Phe Pro Gly Ile Ser Ile Arg Val Asp Ala Ala Phe  
 415 420 425

cag tac aaa gga ttc ttc ttt ttc agc cgt gga tca acg caa ttt gaa 1346  
 Gln Tyr Lys Gly Phe Phe Phe Phe Ser Arg Gly Ser Thr Gln Phe Glu  
 430 435 440 445

tac gac att aag aca aag aat att acc cga atc atg aga act aat act 1394  
 Tyr Asp Ile Lys Thr Lys Asn Ile Thr Arg Ile Met Arg Thr Asn Thr  
 450 455 460

tgg ttt caa tgc aaa gaa cca aag aac tcc tca ttt ggt ttt gat atc 1442  
 Trp Phe Gln Cys Lys Glu Pro Lys Asn Ser Ser Phe Gly Phe Asp Ile  
 465 470 475

*Fig. 2C*

aac aag gaa aaa gca cat tca gga ggc ata aag ata ttg tat cat aag 1490  
 Asn Lys Glu Lys Ala His Ser Gly Gly Ile Lys Ile Leu Tyr His Lys  
 480 485 490

agt tta agc ttg ttt att ttt ggt att gtt cat ttg ctg aaa aac act 1538  
 Ser Leu Ser Leu Phe Ile Phe Gly Ile Val His Leu Leu Lys Asn Thr  
 495 500 505

tct att tat caa taaattcata gacctaaaat aaacctcaac aggtcttttta 1590  
 Ser Ile Tyr Gln  
 510

atataaattc tgcttcaaaa tagaataaaa ccattcttta acaacaagtt gctggtccta 1650  
 gttctaaata tccaaattca atggccattt tgagctgcct gattctttta ataggaagtt 1710  
 attatgtaga aacaaaaatc tctgactgta cttaagcct atttcatgct ttgtggactt 1770  
 ggagaagaca tgtcttataa ctgaatactg aaacatttat taaaccaatc ttttagcattc 1830  
 tg 1832

*Fig. 2D*

Leader Peptide

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1  M---K-----RLLLFLFFITSSAFPLVR---MM---E-----NEENVQL-AQAYLNQFYSLIEGHNHLVQSK-NRSLIDDKIREMQ
1  .HSFP-----P-.L.WGVV.HS..ATL---ET---QEQ-DV-----D-.V.K..EKY.N.KND.RQVEKRR-.SGPVVE.LKQ..
1  .FSL-----T.PF.L.LHVQI.K...-V---SS---KEK-NT-----KT-V.D..EK.Q.PSNQVQSTRKN-GTNV.VE.LK...
1  .HPGV-----LAAF...SWTH-CR.L..PS---GG---DED-DLS..DL.F-.ER..RSY.H-PTNLAGILKEN-AA.SMTERL...
1  .-----TV.CAV-CLLPGSLA.PL---PQ---AG-GMS.LQWEQ---D..KR..LYDS.TKNA-----NSLEA.LK...
1  .K-----F..IL.LQA.A.G.L..NS---ST-----SLEKN..LF-GER.EK.G...NKLPTVKM.YSGN.MKE..Q...
1  .-----S.P.I.L.LCVAVC..Y..DG---AA---RGE-DTS---MN-.V.K..ENY.D.KDKVKQF.RR.-DSGPVVK...
1  .-----M-----H.AF.V.LCLPVC..Y..SG---AA---KEE-DS..-KD.-...Q..EKY.N..KDKVKQF.RR.-DSN..VK..QG..
1  .APAAW-----LRSAAAR.LLPPMLLLL-----QPPPL.AR--A.PPDVH..HAERRGPQWHAALPSSP
1  .SPAPRPP-----RCLL.PLLTLGTALASLG---SAQSSFSPE.W.Q.YGY.PPGDLRHTHTQR-SPOQSLAA.AA..
1  .GSDPSAPGRPGWTGS.LGDREEAARPL.PLLLV--LLGCLGLGVA.A.DAEVH.ENW.RLYGY.PQPSR.MSTM-SAQILASALA...
1  .ILLTFSTGRR-----LD.VHSG-----VFFLQTLWLILCATVCGTEQYFNVEW.QKYGY.PPTDPRMSVVR-SAETMQSALAA..
1  .QQFGG-----LEA.G-----I-----DEATL-----
1  .NCOQLWLG-----FLLP.TVSGRVLGLA.---VAPVD..S.YGY.QKPLE--GSNNFKPED.TEAL.AF.
1  .HPGV-----LAAF...SWTH-CR.L..PS---GG---DED-DLS..DL.F-.ER..RSY.H-PTNLAGILKEN-AA.SMTERL...
1  .-----DPGTV-----
1  .GRGARVPS-----EAPGAGV.RRW.G.A--VALCL.PA---LVLLARLGAPAVPAW-----
1  .EALMARGALTGP.RA.C.LGCLL.H.AAAPS---PIIKFPGD-VAPKTDKE.-VQ..T..GCPK.SCN.-----FVLK.TLKK..
1  .---SLWQPL---V.V.LVLGCC.AAPRQRQS---TLVLFPGDLRT.LTDR..-EE..YRY-----GYTRVAEMRGESKSLGPALLLL.
    
```

contig 355 long  
 contig 355 short  
 COLL1HUM.PRO  
 COLL2HUM.PRO  
 COLL3HUM.PRO  
 MATRHUM.PRO  
 METAHUM.PRO  
 STOIHUM.PRO  
 STO2HUM.PRO  
 STO3HUM.PRO  
 MTM1HUM.PRO  
 MTM2HUM.PRO  
 MTM3HUM.PRO  
 MMP 17P  
 MMP 18P  
 MMP 20P  
 MMP 21P  
 MMP 22P  
 GELAHUM.PRO  
 GELBUM.PRO

Cystine switch

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68  AFFGLTVTGRLDSENTLEIMKTPRCGVPD-----VGQYG-----Y--TLPGWRKYNLTyrIINYT--PDMARAANVDEAIQEGLEWWSKVT
68  .-----
69  E...K...KP.AE.KV.Q.....A.FV-----LTEGN.R.EQTH....E...-LP.D.H.EKAFQL.N..
68  R...N...KPNEE.DM.K.....S.GFM-----LTPGN.K.ERT.....R...-QLSE.E.ER..KDAF.L..VAS
73  S....E...K.D..DV.K.....E.N-----VFPRTLK.S.M.....V...-THSE.EK.FKKAFAK...D..
    
```

contig 355 long  
 contig 355 short  
 COLL1HUM.PRO  
 COLL2HUM.PRO  
 COLL3HUM.PRO

Fig. 3A

# FIG. 3A

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64 K...PI..M.N.RVI...QK.....AE.S-----LFPNS.K.TSKW...VS.--R.LPHIT..RLVSKA.NM.G.EI MATRHUM.PRO
69 H.L.K...Q.TS..M.HA.....HHFR-----EMPGG.V..HYI...N...N...N.ED..Y..RKAFAQ..N... METAHUM.PRO
69 K.L.E...K..D..V.RK.....HFR-----TFPGI.K..TH...V...L.PKD...S.VEKA.K..EE... STO1HUM.PRO
68 K.L.E...K..TD..V.RK.....HFS-----SFPGM.K..TH...V...L.P.D...S..EKA.K..EE... STO2HUM.PRO
60 ---APATQEAAPRASSLRP.....PSDGLSA---RNRQKRFVLSGGR.E.TD.....LRFPW---QLVQEQ.RQTMA.A.K..D... STO3HUM.PRO
70 K.Y.Q...KA.AD.MKA.RR.....KFGAEIKANVRR--KR.AIQGLK.QHNEI.FC.Q...--KVGEY.TY...RKAFA..ESA. MTM1HUM.PRO
88 R.Y.IP...V.EE.K.W..R.....QFGVRVKANLRRRKR.AL.GRK.NNH..FS.Q...--EKLGWYHSM..VRRAFR..EQA. MTM2HUM.PRO
78 Q.Y.INM..KV.R.IDW..K.....Q--TRGSSKFHIRRKR.AL.GQK.QHKHI..S.K.V.--KVGDPETRK..RRAFD..QN... MTM3HUM.PRO
19 -----AL...SL...LPVLTQ---ARRRRQ-APATK.N.R..SW.VRTFPRDSPLGHD.T.RALMYA.K..DIA MMP 17P
62 EASE.P.S.Q..DA.RAR.RQ...LE.P-----FNQKTLK.LLLG-R..KH..F..L.LP--STLPPHTARA.LRQAFQD..N.A MMP 18P
73 S...E...K..D..DV..K.....E.N-----VFPRTLK.S.M.....V...THSE.EK.FKAKF...D... MMP 20P
7 -----AT.RK...SL..VLGVAGL---VRRRRR.ALGSV.K.RT..W.VRSFPQSSQLSQET.RVLMSYA.MA.GMES MMP 21P
49 -----SAAQG.VAA.GLSAV.PTR..GPLAP-----RRRRYTLTPARLR.DHL.....LSFPRNL-LSPRETRR.LAAAFRM..D.S MMP 22P
79 K...PQ..D..Q..I.T.RK...N.....AN.N-----FFPRK.K.D.NOI.....G...LDPET..D.FARAFQ...D... GELAHUM.PRO
76 KQLS.PE..E...A..KA.R.....L.RFQ-----TFEGDLK.HHH.I..W.Q..S--E.LP..VI.D.FARAFAL..A... GELBHUM.PRO
    
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## Second Zn++ and Ca++ binding domain

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143 PLKFTKI-----SKGIADIMIAFRTRVHGRC-----PRYFDGPLGLVGHAFPPGPG-LGGDTHFDEDENWTKDGA----- contig 355 long
143 ..... contig 355 short
146 ..T..V-----E.Q...S.VRGD.RDN-----SP-...G.N.A..Q...-I..A.....R..NNFR----- COLL1HUM.PRO
145 ..I..R-----Q.E..N..YQ.D.DN-----SP-...N.I.A..Q..Q..I..A..AE.T..NTS----- COLL2HUM.PRO
150 ..N..RL-----HD...S.GIKE..DF-----YP-...S.L.A.....N-Y..A..D..T..SSSK----- COLL3HUM.PRO
141 ..H.R.V-----VW.T...G.ARG.A..DS-----YP-...GNT.A..A..T...A.....R..DGSSSLGIN----- MATRHUM.PRO
146 ...S.....NT.M..LVV.ARG.A..DF-----HA-...KG.I.A..G..S..I..A.....F..THSG----- METAHUM.PRO
146 ..T.SRL-----YE.E...S.AV.E..DF-----YP-...GN..A..YA...-IN..A..D..Q...TT----- STO1HUM.PRO
145 ..T.SRL-----YE.E...S.AVKE..DF-----YS-...GHS.A..Y...-Y..I..D..K..E.AS----- STO2HUM.PRO
142 ..T..E-----V---HE.R...D.ARYWD.DD-----LP-...G.I.A..F.KTHR-E..V..Y..T..IG--D----- STO3HUM.PRO
156 ..R.REVPYAYIREGHEKQ.....F.AEGF..DS-----TP-...EG.F.A..YF..N-I.....SA.P..VRNEDL----- MTM1HUM.PRO
    
```

Fig. 3B

Fig. 3C



194	-----Ysw-----	MMP 22P
231	EYCKFPFLFNGKEYNSCTDTRSDGFLWCSTTYNFEKDKYGFPCHEALFTMGNAEQCKPFRFQGTSDCTTEGRTDGYRWCGTT	GELAHUM.PRO
228	AACHFPFIFEGRSYSACTTDGRSDGLPWCSTTANYDTRDRFGFCPSERLYTRDGNADGKPCQFPFIFQGSYSACTTDGRSDGYRWCAAT	GELBHUM.PRO
207	-----GFNLFLVAHFEFGHAL	contig 355 long
164	-----	contig 355 short
209	-----EY.HR....L.S.	COLL1HUM.PRO
208	-----NY.....S.	COLL2HUM.PRO
213	-----Y.....S.	COLL3HUM.PRO
212	-----T.L.S.	MATRUM.PRO
209	-----T...T.V.I.S.	METAHUM.PRO
209	-----T.....I.S.	STO1HUM.PRO
208	-----T.....L.S.	STO2HUM.PRO
204	-----DQ.TD.LQ.....V.	STO3HUM.PRO
229	-----N.NDI....V.L....	MTM1HUM.PRO
249	-----H.N.....V.L....	MTM2HUM.PRO
236	-----D.ND.....V.L....	MTM3HUM.PRO
153	-----AH.MD..A.V.....I	MMP 17P
203	-----V.RII....V....	MMP 18P
213	-----Y.....S.	MMP 20P
146	-----SQGLE-----Q.LAGG-	MMP 21P
197	-----KKGW-----LTD.VH....I....	MMP 22P
321	EDYDRDKKYGFPCETAMSTV-GGNSEGAPCVFPFTFLGNKYESCTSAGRSDGKMGWCAATANYDDDRKMGFCPDQ.YS.....M	GELAHUM.PRO
318	ANYDRDKLFGFCPTRADSTVMGNSAGELCVFPFTFLGKEYSTCTSEGRDGLWCATTSNFDSDKKMGFCPDQ.YS.....	GELBHUM.PRO

Fig. 3D

# FIG. 3E

Zn++ binding domain			
223	GLSHNDQTALMFPNYVS-L-DPRKYPLS--QDDINGIQSIYGG--LPKEPAKPEKTIP----		contig 355 long
180	.....		contig 355 short
225	.....T.IG...Y.S.-T-F--SGDVQ.A--...D...A...RSQNPVQ-----IG.QT.		COLL1HUM.PRO
224	.....A..S.PG...Y...-A-FRETSN.S.P--...D...A...LSSNPIQ-----TG.ST.		COLL2HUM.PRO
229	.....D..K.PG....I.-T-YTGKSHFM.P--D..VQ...L..PGDE-----DPN..H.KT.		COLL3HUM.PRO
221	.....MG..S.PN.V.Y.T.-G-NG..QNFK...K..KL-----		MATRHUM.PRO
225	.....G..S.PK.V...T.K--YV.INTFR.--A...R...L..DPKENQRLP-----NPDNSE.		METAHUM.PRO
225	.....F..ANTE...Y.L.H.-.T.LTRFR.....L..PPDSPETP.VPTEPV.P..GT.		STO1HUM.PRO
224	.....F..ANTE...Y.L.N.-FTELAQFR.....V...L..PPPASTEETP.VPTKSV.SGSEM.		STO2HUM.PRO
222	.....Q..TTAAK...SAF-----TFR...LSP..CR.V.HL..QP--WPTVTSRT-----		STO3HUM.PRO
246	.....E..S.PS.I.A.F.Q--WM.TENFV.P--D..RR...QL...ESG-----FPTKM.PQ.-RT-SRPSVPDKPKNPT-----		MTM1HUM.PRO
266	.....E..SNPN.I.A.F.Q--WK.VDNFK.P--E..LR...QL..TPDGQPQTQ.LPTVT.RR.GR.-DHRPPRPQPPPGGKPERPPKP		MTM2HUM.PRO
254	.....E....P..I.A.F.Q--YME-QTLQ.P--N..YR--HQR.MSPDKIPPTR.LPTV.-PHRS.-PADPRKNDRKPPRPPTGRPSYP		MTM3HUM.PRO
171	.....VAAAHSI.R.Y.QGPVG..LR.G.PYE-.KVR-VWQL..VRESVSPTAQ.E-----		MMP 17P
219	.....G..RYSQ...A.V.EG--YRPHFK.H--P..VA...AL..KKSPVIRDEEEE.TEL.TV.PV.TEPS-----		MMP 18P
229	.....D..K.PG....I.-T-YTGKSHFM.P--D..VQ...L..PGDE-----DPN..H.KT.		MMP 20P
157	.....PVDEELGFS-----		MMP 21P
218	.....M..QHGR.....-H.NATLRGWKALS..ELW.LHRL..C-----LDRLFVCASWARRGF-----		MMP 22P
410	.....E..Q.PG...A.I.-T-YT--KNFR.....K...EL..ASPD--ID.GTG.TPTLG.VT-----		GELAHUM.PRO
408	.....D..SVPE...Y.M.R--FTEGP--H--K..V...RHL..PRPEPRPPTTTTPQ.TA.PTVCPTGPPTVHPSERPTAGTGPSPA		GELBHUM.PRO
277	-----HACD--PDLTFDAITTFRREVWFFKGRHLWR-IYYDITDVE-FELIASFWPSLP---ADLQAAYENP-		contig 355 long
234	-----		contig 355 short
276	-----K...-SK.....I.G....D.FYM.-TNPFYPE..LNF.SV...Q...-NG.E...FAD		COLL1HUM.PRO
277	-----KP...-S...L.G.IL..D.YF.-RHPQLQR..-MNF.SL.....-TGI...DFD		COLL2HUM.PRO
282	-----DK...-S.SL...SL.G.T.I..D.FF.-LHPQQV.A.-LF.TK...E...-NRID...H.S		COLL3HUM.PRO
259	-----		MATRHUM.PRO

Fig. 3E

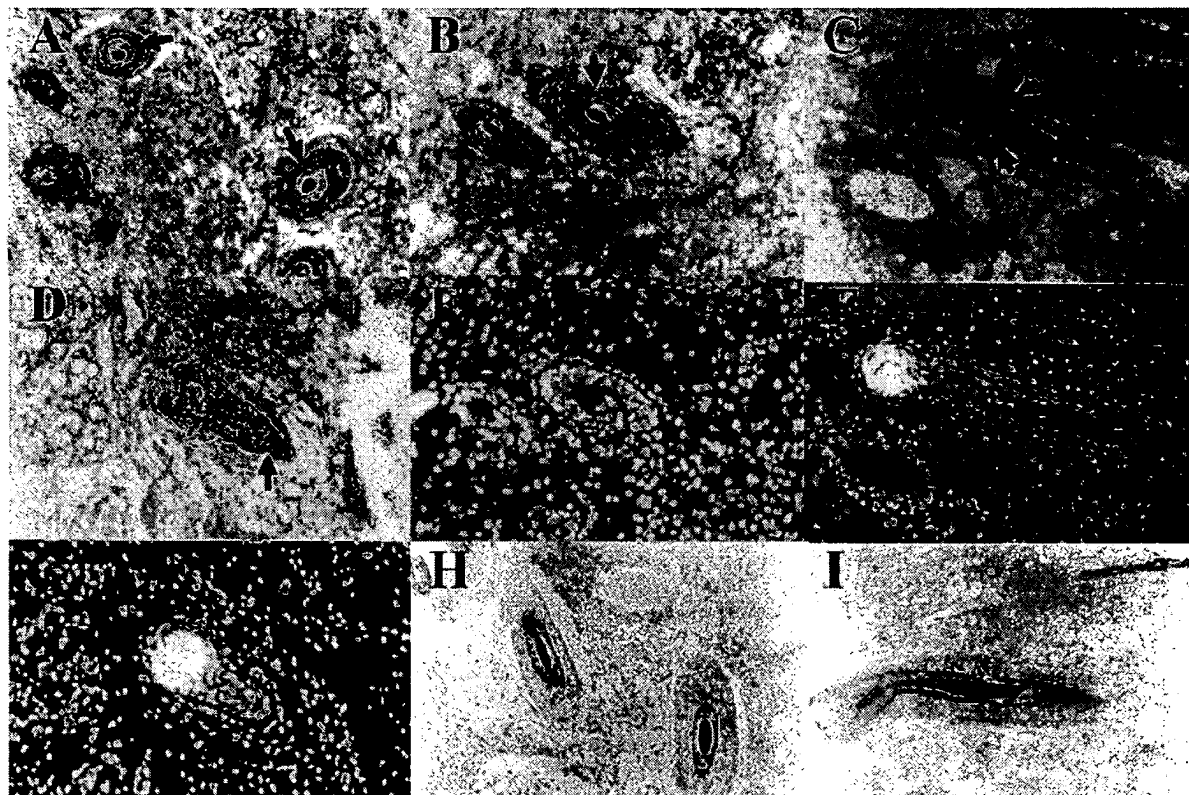
102040" 05110550

280	-----AL.---.N.S...V..VGNKIF...D.FF.L-KVSRPKTS-VN..S.L..T.---SGIE....IEA	METAHUM.PRO
288	-----AN.---.A.S...VS.L.G.ILI..D..F..-KSLRKLEP..-LH..S.....-SGVD....VTS	STO1HUM.PRO
287	-----AK.---.A.S...S.L.G.YL..D.YF..-RSHWNEP..-H..SA.....-SY.D....VNS	STO2HUM.PRO
269	-PALGPQAGIDTNEIAPLEDPAPDA--CEAS...VS.I.G.LF..AGFV..L-RGGQLQGYPA.ASRH.QG.---SPVD..F.DAQ	STO3HUM.PRO
314	-----YGP-----NI.---GN--..TVAML.G.MFV..E.WF..VRNQVM.GYMPM-.GQ..RG.---SINT...RKD	MTM1HUM.PRO
351	GPPVQPRATERPDQYGP-----NI.---G.---TVAML.G.MFV....WF..VRHNRVL.NYPMP-.GH..RG.---G.IS....RQD	MTM2HUM.PRO
334	GAK-----P-----NI.---GN--..NTLAIL...MFV..DQWF..VRNRMV.GYPMQ-.TY..RG.---PSID.V...SD	MTM3HUM.PRO
225	-PPLLPEPPDNRSSAPP--RKDVPHR--CSTH...VAQI.G.AF...KYF..LTRDRHLVSLQPAQMHR..RG..LHLSVD.V..RTS	MMP 17P
285	-----MPDP.S--SE.D-AMMLGP.GKTYA...DYV.TVSDS---GPGPLFRVSAL.EG..GNLD--A.V.S-.R	MMP 18P
282	-----DK.---.S.SL...SL.G.T.I..D.FF..-LHPQQV.A.-LF.TK...E.---NRID....H.S	MMP 20P
167	-----G-----RVN.L-----	MMP 21P
271	-----CDARRRLMKRLCP--SS..FCYEFP.PTVA.TPPPP-----TKTRLVPEGRNWTFRCG-----	MMP 22P
467	-----EI.K--Q.IV..G.AQI.G.IF...D.FI..TVTPRDKPMG-PL.V.T..E.---EKID.V..A.Q	GELAHUM.PRO
492	GPTGPPTAGPSTATTVPLSPVDD..N--VNI-....AEIGNQLYL..DGKY..FSEGRGSRPQGP...DK.A.---RK.DSVF.E.L	GELBHAM.PRO

342	RDKILVFKDENFWMIRGYAVL PDYPKSIHT-LGFPGRVKKIDAANVCDK-TTRKTYFFVGWCFDEMTQTMDKGFQQRVVKHFPGISIR	contig 355 long
294	.....	contig 355 short
337	..EVRF..GNKY.AVQ.QN..HG...D.YSSF...RT..H...LSEE-N.G.....ANKY..Y..YKRS..P.Y.KMIAHD....GHK	COLL1HUM.PRO
338	..L.FL..GNQY.ALS..DI.QG...D.-SNY...SS.OA...F---YRS.....NDQF..Y.NQR.F.EP.Y.KSISGA....ESK	COLL2HUM.PRO
343	H.L.FI.RGRK..ALN..DI.EG...K.-SE..L.KE....S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED....GDK	COLL3HUM.PRO
261	-----KRS-NS..K-----	MATRUM.PRO
341	.NQVFL...DKY.L.SNLRPE.N...S-F...NF.....FNP-RFYR....DNQY..Y..RR.M..P.Y.KLIT.N.Q..GPK	METAHUM.PRO
349	K.LVFI..GNQ..A...NE.RAG..RG...PT.R...IS..-EKN....EDKY....KRN.S.EP..KQIAED....DSK	STO1HUM.PRO
348	..TVFI..GNE..A...NE.QAG..RG...PTIR....S.-EKK....AADKY....NS.S.EQ...RLIADD...VEPK	STO2HUM.PRO
352	GH-.WF.QGAQY.VYD.EKPVLG-.APL-.E..LVREF--VH..LVWGPEKN.I...R.RDY...HPS.RRV.SPV.R.ATD-WR.VPSE	STO3HUM.PRO
377	GKFVF-..GDKH.VFDEASLE.G...H.-KE..RGLPTD....LFWM-PNG.....R.NKYY..N.ELRAV.SEY.KNIKV-WE..PES	MTM1HUM.PRO
428	GRFVF-..GDRY.LF.EANLE.G..QPL-.SY.LGIPYDR..T.IWWE-P.GH.F..QEDRY...N.E..RG.P.Y.KPISV-WQ..PAS	MTM2HUM.PRO
398	GNFVF-..GNKY.VFKDITLQ.G..HDL-IT..SGIPPHG..S.IWWE-DVG....K.DRY..YS.EMK...P.Y.KPITV-WK..PES	MTM3HUM.PRO

Fig. 3F



A-G: Antisense RNA probe for human MMP 25

H and I: Sense RNA probe for human MMP 25

Arrows in A, B, C, and D highlight cells in the hair follicle that express MMP 25 message

Cell nuclei are counterstained with H33258 in E, F, and G.

*Fig. 5*

Fig. 36

310	DH..VF..GDRY.VFKDNN.EEG..RPV-SDFS.L.PGG--...	FSWA-HNDR....KDQLY..Y.DH.RH..P.Y.AQSPL-WR.VPST	MMP 17P
356	TQM.HF..GDKV.RYINFMS.GF..KLN-----RSEPNL...	LYW-PLNQ.VFL.K.SGY.QW..LAR.DFSSY.KPIKGL.T.VPNQ	MMP 18P
343	H.L.FI.RGRK..ALN..DI.EG..K-SE..L.KE...S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED....GDK		MMP 20P
174	-----		MMP 21P
323	-Q...HK.GKVY..-----KQEPLEFSY..-----	YLALGEA.LSI.ANA	MMP 22P
529	EE.AVF.AGNEY.IYSASTLERG...PL-.S..L.PD.QRV...FNWS-KNK...I.A.DKF..YN.VKKK..P...KLIADAMNA.PDN		GELAHUM.PRO
576	SK.LFF.SGRQV.VYT.AS..G--.RRLD-K..LGAD.AQVTG.LR-S-GRG.MLL.S.RRL....VKA.MV.PRSASE.DRM....VPLD		GELBHAM.PRO
425	VDAAFAQK--GFF----FFSRGSTQFEYDIKTKNITRIMRTNT-----WFQCKEP-----		contig 355 long
382	-----		contig 355 short
426	...V.--MKD...----Y.FH.TR.YKF.P...R.LTLQA.S-----N.RKN		COLL1HUM.PRO
424	...V.--QKEH...----HVFS.PRYAF.LIAQRV..VA.G.K-----LN.RYG		COLL2HUM.PRO
431	...VY--EKN.YI----Y.FN.PI.....S.WSNR.V.V.PA.S-----ILW.		COLL3HUM.PRO
267			MATRHUM.PRO
429	I..V.-.SKNKYY----Y.FQ..N.....FLLQR..KTLKS.S-----G.		METAHUM.PRO
437	I..V.--EEF...----Y.FT..S.L.F.PNA.KV.HTLKS.S-----LN.		STO1HUM.PRO
436	...VL--QAF...----Y.FS..S...F.PNARMV.H.LKS.S-----LH.		STO2HUM.PRO
436	I.....DADGY----AY.L..RLYWK.F.PVKVKALE-GFRLVGP.DF.G.A..ANTLL		STO3HUM.PRO
463	PRGS.MGSDEV.----TY.YK.NKYWKFNQKL-KVEPGYKPSALRD.MG.-----PSGGRP-----DEGTEETEVIIEVDEEG		MTM1HUM.PRO
514	PKG..LSNDAAY----TY.YK.TKYWK.F.NERL-RMEPGYKPSILRDFMG.Q.HVEPGRPWDVARPPFNPHGGAEPGADSAEGDVGDDG		MTM2HUM.PRO
484	PQG..VH.EN...----TY.YKEGVL-.IQTRYSRLEPGHPRSILKOLSG.D---GPTDRVKEGHSP-----DDVD---		MTM3HUM.PRO
395	L.D.MRWSDGA----SY.F..QEYWKVLDGELEVAP-GYPQSTARD.LV.GDSQADGS-----VAAGVDAEGRAPPQGHDQSR		MMP 17P
429	PS..MSWQDG-----RVY.FK.KVYWRLN-QQLRVEKGYPRNISHN.MH.RPRTIDTTPSGGNTTPS-----		MMP 18P
431	...VY--EKN.YI----Y.FN.PI.....S.WSNR.V.V.PA.S-----ILW.		MMP 20P
175	-----		MMP 21P
363	.N-----EGTYTC-----WRRQQRVLTTYSMRVRVRG		MMP 22P
617	L...VVDLQGG.HS----Y.FK.AYYLKLENQSLKSVKFGSIKS--D.LG.		GELAHUM.PRO

Fig. 36

661 660 659 658 657 656 655 654 653 652 651 650 649 648 647 646 645 644 643 642 641 640 639 638 637 636 635 634 633 632 631 630 629 628 627 626 625 624 623 622 621 620 619 618 617 616 615 614 613 612 611 610 609 608 607 606 605 604 603 602 601 600 599 598 597 596 595 594 593 592 591 590 589 588 587 586 585 584 583 582 581 580 579 578 577 576 575 574 573 572 571 570 569 568 567 566 565 564 563 562 561 560 559 558 557 556 555 554 553 552 551 550 549 548 547 546 545 544 543 542 541 540 539 538 537 536 535 534 533 532 531 530 529 528 527 526 525 524 523 522 521 520 519 518 517 516 515 514 513 512 511 510 509 508 507 506 505 504 503 502 501 500 499 498 497 496 495 494 493 492 491 490 489 488 487 486 485 484 483 482 481 480 479 478 477 476 475 474 473 472 471 470 469 468 467 466 465 464 463 462 461 460 459 458 457 456 455 454 453 452 451 450 449 448 447 446 445 444 443 442 441 440 439 438 437 436 435 434 433 432 431 430 429 428 427 426 425 424 423 422 421 420 419 418 417 416 415 414 413 412 411 410 409 408 407 406 405 404 403 402 401 400 399 398 397 396 395 394 393 392 391 390 389 388 387 386 385 384 383 382 381 380 379 378 377 376 375 374 373 372 371 370 369 368 367 366 365 364 363 362 361 360 359 358 357 356 355 354 353 352 351 350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305 304 303 302 301 300 299 298 297 296 295 294 293 292 291 290 289 288 287 286 285 284 283 282 281 280 279 278 277 276 275 274 273 272 271 270 269 268 267 266 265 264 263 262 261 260 259 258 257 256 255 254 253 252 251 250 249 248 247 246 245 244 243 242 241 240 239 238 237 236 235 234 233 232 231 230 229 228 227 226 225 224 223 222 221 220 219 218 217 216 215 214 213 212 211 210 209 208 207 206 205 204 203 202 201 200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 0

661 THDV...REKAY.CQDR.YW.V.SRS.LN-----QVDQVGIVTY---DIL..P.D

471 SSFGFDINKEKAHSGGIK-----ILYHKSLSFI-----FGIVHLLKNTS----IYQ

428 .....

426 .....

424 .....

431 .....

267 .....

429 .....

437 .....

436 .....

436 .....

536 GG-----AVSAAVLPVL.L.LVLAVGLAVFFRRHGTPrLL.C.RSLLDKV

599 GD..AGV..DGGSRVVQMEEVARTVNVWV.VPLL.L.CVLGLTYAL.QMQRKGAPrVLL.CKRSIQEW

548 -----IV..LDNTASTVKAIA.VIPCI.A.CLLVLVYTVFQFKRGTPRHIL.CKRSMQEW

470 .ED.YEVCSTS-----GASSPPGAPG.VAATML.LLPPL-----PGALWTAQAQALT--L

488 -----GT..TLDTILSATETT-----FEY

175

363

617

661

GELBHUM.PRO

contig 355 long

contig 355 short

COLL1HUM.PRO

COLL2HUM.PRO

COLL3HUM.PRO

MATRUM.PRO

METAHUM.PRO

ST01HUM.PRO

ST02HUM.PRO

ST03HUM.PRO

MTM1HUM.PRO

MTM2HUM.PRO

MTM3HUM.PRO

MMP 17P

MMP 18P

MMP 20P

MMP 21P

MMP 22P

GELAHUM.PRO

GELBHUM.PRO

Fig. 3H

stimulated PBL  
fetal skin  
cartilage  
adipose tissue  
bone  
PBL  
ovary  
umbilical cord  
parotid  
thyroid  
salivary gland  
pancreas  
adrenal gland  
placenta  
spinal cord  
fetal liver  
fetal brain  
cerebellum  
brain  
trachea  
lung  
liver  
kidney  
skin  
thymus  
stomach  
spleen  
sm. intestine  
colon  
bone marrow  
uterus  
testis  
skel. muscle  
prostate  
mammary gland  
heart

Fig. 4